



SEQUENCE LISTING

<110> Japan Patent and Technology Agency

<120> Transcriptional regulator ZHX3

<130> FS03-323PCT

<160> 35

<170> PatentIn version 3.1

<210> 1

<211> 956

<212> PRT

<213> Homo sapiens

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35 40 45

Ser Ser Glu Ala Ala Gln Asn Pro Ser Ser Thr Asp Gly Ser Thr Leu

50 55 60

Ala Asn Gly His Arg Ser Thr Leu Asp Gly Tyr Leu Tyr Ser Cys Lys

65 70 75 80

Tyr Cys Asp Phe Arg Ser His Asp Met Thr Gln Phe Val Gly His Met

85 90 95

Asn Ser Glu His Thr Asp Phe Asn Lys Asp Pro Thr Phe Val Cys Ser

100 105 110

Gly Cys Ser Phe Leu Ala Lys Thr Pro Glu Gly Leu Ser Leu His Asn

115 120 125

Ala Thr Cys His Ser Gly Glu Ala Ser Phe Val Trp Asn Val Ala Lys

130 135 140

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Lys Ala Glu Ala Lys Lys Ile His Thr Leu Lys Glu Asn Val Pro Ser
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Gln Pro Val Gly Glu Ala Leu Pro Lys Leu Ser Thr Gly Glu Met Glu
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Val Arg Glu Gly Asp His Ser Phe Ile Asn Gly Ala Val Pro Val Ser
225 230 235 240
Gln Ala Ser Ala Ser Ser Ala Lys Asn Pro His Ala Ala Asn Gly Pro
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Asn Ser Phe His Lys Phe Pro Tyr Pro Thr Lys Ala Glu Leu Cys Tyr
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Glu Leu Asp Arg Leu Arg Ser Glu Thr Lys Met Thr Arg Arg Glu Ile
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Asp Ser Trp Phe Ser Glu Arg Arg Lys Lys Val Asn Ala Glu Glu Thr
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675 680 685
Asp Glu Gly Gly Glu Glu Asp Leu Ala Ser Glu Leu Arg Val Ser Gly
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705 710 715 720
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Asp Asp Glu Ser Asn Lys Leu Ala Glu Gln Leu Pro Gly Lys Val Ser
755 760 765
Cys Lys Lys Thr Ala Gln Gln Arg His Leu Leu Arg Gln Leu Phe Val
770 775 780
Gln Thr Gln Trp Pro Ser Asn Gln Asp Tyr Asp Ser Ile Met Ala Gln
785 790 795 800
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His Lys Gly Met Gly Asp Thr Tyr Ser Glu Val Ser Glu Asn Ser Glu
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35 40 45
Ser Val Leu Ala Gly Glu Ser Thr Glu Gly Thr Glu Ile Ile Ile Thr
50 55 60
Lys Thr Pro Ile Met Lys Ile Met Lys Gly Lys Ala Glu Ala Lys Lys

65 70 75 80
Ile His Met Leu Lys Glu Asn Ala Pro Thr Gln Pro Gly Gly Glu Ala
85 90 95
Leu Pro Lys Pro Leu Ala Gly Glu Thr Glu Gly Lys Glu Gly Asp His
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Thr Phe Ile Asn Gly Ala Thr Pro Val Ser Gln Ala Ser Ala Asn Ser
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Thr Lys Pro Pro His Thr Ala Asn Gly Pro Leu Ile Gly Thr Val Pro
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Val His Pro Gln His His Pro His Gln Pro Leu Pro Thr Ser Lys Ala
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Leu Pro Lys Val Met Ile Pro Leu Ser Ser Ile Pro Thr Tyr Asn Ala
180 185 190
Ala Met Asp Ser Asn Ser Phe Leu Lys Asn Ser Phe His Lys Phe Pro
195 200 205
Tyr Pro Thr Lys Ala Glu Leu Cys Tyr Leu Thr Val Val Thr Lys Tyr
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Pro Glu Glu Gln Leu Lys Ile Trp Phe Thr Ala Gln Arg Leu Lys Gln
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Gly Ile Ser Trp Ser Pro Glu Glu Ile Glu Asp Ala Arg Lys Lys Met
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Phe Asn Thr Val Ile Gln Ser Val Pro Gln Pro Thr Ile Thr Val Leu
260 265 270
Asn Thr Pro Leu Val Ala Ser Ala Gly Asn Val Gln His Leu Ile Gln
275 280 285
Ala Ala Leu Pro Gly His Ala Val Gly Gln Pro Glu Gly Thr Ala Gly
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Gly Leu Leu Val Thr Gln Pro Leu Met Ala Asn Gly Leu Gln Ala Ser
305 310 315 320
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325 330 335
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340 345 350
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355 360 365
Gln Ala Phe Leu Asp Ala Asn Ile Tyr Lys Asn Lys Lys Ser His Glu
370 375 380
Gln Leu Ser Ala Leu Lys Gly Ser Phe Cys Arg Asn Gln Phe Pro Gly
385 390 395 400
Gln Ser Glu Val Glu His Leu Thr Lys Val Thr Gly Leu Ser Thr Arg
405 410 415
Glu Val Arg Lys Trp Phe Ser Asp Arg Arg Tyr His Cys Arg Asn Leu
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Lys Gly Thr Arg Ala Met Val Pro Gly Glu His Gly Ser Val Leu Ile
435 440 445
Asp Ser Val Pro Glu Val Pro Phe Pro Leu Ser Ser Lys Val Pro Glu
450 455 460
Val Pro Cys Val Pro Thr Ala Thr Ser Leu Val Ser His Pro Ala Thr
465 470 475 480
Lys Arg Gln Ser Trp His Gln Thr Pro Asp Phe Thr Pro Thr Lys Tyr
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